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FEATURES
  source      1..18
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BASE COUNT   2 a      5 c      7 g      4 t
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Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGTGGTCCAGCCGTA 18
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       1 GTGGTGGTCCAGCCGTA 18

RESULT 2
LOCUS      AR098113 218 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6074832.
ACCESSION  AR098113
VERSION     AR098113.1 GI:12807370
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 218):
            Venter, P.J., Brewer, G.J., Yuzbasyan-Gurkan, V., Schall, W.D. and
            Dufrenoy, J.
            DNA encoding canine von Willebrand factor and methods of use
            Patent: US 6074832 A 21 12-1999
FEATURES
  source      1..218
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BASE COUNT   28 a      67 c      74 g      49 t
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Query Match      100.0%; Score 18; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGTGGTCCAGCCGTA 18
       11111111111111111111
       1 GTGGTGGTCCAGCCGTA 190

RESULT 3
LOCUS      H01WVPA04 734 bp DNA linear PRI 14-JAN-1995
DEFINITION Human von Willebrand factor gene, exon 7.
ACCESSION  M25831 M25716
VERSION     M25831.1 GI:340320
KEYWORDS    coagulation factor VIII; von Willebrand factor
SEGMENT     4 of 38
            Human placenta, leukocyte, fetal liver and cell line EB19 DNA
            clones lambda: [1,2,7,9,11], h[6,7,18], c[1,2,3,4,5,9,14,18] and
            pW[5,8,12,3].
            Homo sapiens.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 734):
            Mancuso, D., Tiller, P.A., Westfield, A., Wotral, N.R.,
            Shelton-Inloes, B.B., Sorace, J.M., Alevis, Y.G. and Sadler, J.E.
            Structure of the gene for human von Willebrand factor
            J. Biol. Chem. 264 (33), 19514-19527 (1989)
JOURNAL     90062044
MEDLINE     258182
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by J.E.Sadler, 30-JUN-1989.
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ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGTGGTCCAGCCGTA 18
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       1 GTGGTGGTCCAGCCGTA 298

RESULT 4
LOCUS      HSWMF 4429 bp mRNA linear PRI 21-MAR-1995
DEFINITION Human mRNA fragment (5' terminus) for von Willebrand factor (VWF).
ACCESSION  X04146
VERSION     X04146.1 GI:37941
KEYWORDS    Glycoprotein; plasma protein; signal peptide; von Willebrand
            factor.
SOURCE      Homo sapiens.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 4429):
            Verweij, C.L., Diegaerde, P.J., Hart, M. and Pannekoek, H.
            Full-length von Willebrand factor (VWF) cDNA encodes a highly
            repetitive protein considerably larger than the mature VWF subunit
            EMBO J. 5 (8), 1839-1847 (1986)
JOURNAL     87004569
MEDLINE     3019665
COMMENT     See also
            <HSWMF2> (M10321) corresponding to pos. 2458-2849 and
            (M10320) corresponding to pos. 4894-4429.
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              239..25429
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BASE COUNT 1759 a 2467 c 2559 g 1790 t
ORIGIN

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Query Match 100.0%; Score 18; DB 9; Length 8575;
Best Local Similarity 100.0%; Pred. No. 1,le-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1 GTGGTGGTCGACCGCTA 13
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DB 963 GTGGTGGTCGACCGCTA 946

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RESULT 7
108449/c 108449 8588 bp INA linear PAT 02-DEC-1994
LOCUS
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DEFINITION Sequence 3 from Patient W0 8606096.
ACCESSION 108449
VERSION 108449.1 GI:5888840
KEYWORDS
SOURCE
ORGANISM unknown.
REFERENCE
1 (bases 1 to 8589)
AUTHORS Giesburg D., Orkin S.H. and Kaufman, R.J.
TITLE VON WILLEBRAND FACTOR
JOURNAL Patent: W0 8606096-A 3 23-OCT-1986;
FEATURES
source
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/organism="unknown"
BASE COUNT 1763 a 2472 c 2559 g 1794 t
ORIGIN

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Query Match 100.0%; Score 18; DB 6; Length 8588;
Best Local Similarity 100.0%; Pred. No. 1,le-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 970 GTGGTGGTCGACCGCTA 953

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RESULT 9
AF099154/c 8601 bp mRNA linear MAY 14 JAN 1999
LOCUS AF099154
DEFINITION Canis familiaris von Willebrand factor (VWF) mRNA, complete cds.
ACCESSION AF099154
VERSION AF099154.1 GI:4154308
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 8601)
AUTHORS Venla, P.J., Li, J., Yuzbasizyan-Gurkan, V., Brower, G.J. and
Schall, W.D.
TITLE Complete sequence of the structural gene for canine von Willebrand
factor and identification of a mutation causing Scottish torrier
von Willebrand's disease
JOURNAL Unpublished
2 (bases 1 to 8601)
AUTHORS Venla, P.J., Li, J., Yuzbasizyan-Gurkan, V., Brower, G.J. and
Schall, W.D.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1998) Microbiology, Michigan State University,
College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
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BASE COUNT 1425 A 2436 C 2508 G 1832 T

Query Match 100.0% Score 18; DB 4; Length 8601;
 Best local similarity 100.0%; Prod. No. 11e102;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGTCGTCGACGGCTA 18
 DB 864 GTGGTGTGTACACCGTA 847

RESULT 9
 LOCUS 8654 bp DNA linear MAM 02-Aut-1996
 DEFINITION Canis familiaris von Willebrand factor mRNA, complete cds.
 ACCESSION U76227
 VERSION 1.76227.1 GI:1478045
 KEYWORDS von Willebrand factor.
 SOURCE Canis familiaris
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 8654)
 Stoy,S.O., Shibuya,H., Neumann,D.J., Holzhauer,J., Mohammed,I.H.
 and Johnson,G.S.
 Canine vWF cDNA sequence
 unpublished (1996)
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QY 1 GTCGTCGTCGACGGCTA 18
 DB 864 GTGGTGTGTACACCGTA 847

BASE COUNT 1425 A 2436 C 2508 G 1832 T

Query Match 100.0% Score 18; DB 4; Length 8601;
 Best local similarity 100.0%; Prod. N 11e102;
 Matches 18; Conservative 0; Mismatches 0;

QY 1 GTCGTCGTCGACGGCTA 18
 DB 864 GTGGTGTGTACACCGTA 847

RESULT 10
 LOCUS 8654 bp DNA linear MAM 02-Aut-1996
 DEFINITION Canis familiaris von Willebrand factor mRNA, complete cds.
 ACCESSION U76227
 VERSION 1.76227.1 GI:1478045
 KEYWORDS von Willebrand factor.
 SOURCE Canis familiaris
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 8654)
 Stoy,S.O., Shibuya,H., Neumann,D.J., Holzhauer,J., Mohammed,I.H.
 and Johnson,G.S.
 Canine vWF cDNA sequence
 unpublished (1996)
 FEATURES
 Source location/Qualifiers
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 /db_xref="taxon:9615"
 57..8498
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 3694)
 Montgomerly, R. R., Fells, S. and Montgomerly, M. W.
 Canine vmi
 Unpublished
 2 (bases 1 to 4694)
 Montgomerly, R. R., Fells, S. and Montgomerly, M. W.
 Direct Submission
 Submitted (06-AUG-1996) Blood Research Institute, The Blood Center
 of Southeastern Wisconsin, Box 2178, Milwaukee, WI 53201-2178, USA
 FEATURES
 source
 1 4694
 Location/Qualifiers
 /organism="Canis familiaris"
 /db_xref="taxon:9615"
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 /protein_id="AA03766.1"
 /db_xref="GI:2734858"

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Query Match 100.0%; Score 18; DB 4; Length 8694;
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 Db 968 GTGGTGGTCCAGCGCTA 951

RESULT 11
 AR098096/C
 Length 8694
 DEFINITION Sequence 1 from patent US 6074832.
 ACCESSION Ap098096
 VERSION Ap098096.1 GI:12807353
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 8802)
 Ventura, P. J., Brewer, C. J., Yuzbaysyan-Gurkan, V., Schall, W. D., and
 Duffendack, J. DNA encoding canine von Willebrand factor and methods of use
 Patent: US 6074832-A 1 13-JUN-2000;
 Location/Qualifiers
 1..8802
 /organism="unknown"

BASE COUNT 1886 a 2477 c 2544 g 1495 t
 ORIGIN
 Query Match 100.0%; Score 18; DB 5; Length 8802;
 Best Local Similarity 100.0%; Pred. No. 1; Le-02;
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RESULT 12
 BD000647/C
 Length 8694
 DEFINITION Polypeptide and process for producing polypeptide.
 ACCESSION BD000647
 VERSION BD000647.1 GI:18623760
 KEYWORDS
 Synoptic
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Vertebrata; Furostomii;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 8805)
 Hans, P., Rumberg, P. C., Jovan, P. and Louisa, H. M.
 Polypeptide and process for producing polypeptide
 Patent: JP 2000442740 A 1 12-DEC-2000;
 IMMUNO AG

COMMENT
 OS Homo sapiens (human)
 PN JP 2000442740-A/1
 PD 12-DEC-2000
 PE 18-MAY-2000 JP 2000145965
 PR 01-APR-1985 NL 8500961
 PI PANNAOOCK HANS, PULIVE CORNELIUS RUMERARTZ, DIAHALDA PAUL, JOHAN,
 PI HARTZ MARGARETA HENDRIKA LOUISA
 PC C12N15/009; C07K14.745; C12P21/02; C12N15/710
 CC
 KEY key
 FH source
 FT source
 FT location/Qualifiers
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 /db_xref="taxon:9606"

BASE COUNT 1804 a 2529 c 2525 g 1847 t

SOLITE	HOHO	SAPIENS.
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CHRISTIANISM

1 (bases 1 to 116840)

AUTHORS
 GANTU, L.A. and ROE, B.A.
 TITLE
 Homo sapiens Chromosome 12p13.3 BAC Clone 762c12
 JOURNAL
 Unpublished

2 (bases 1 to 116840)
McDermid H. F.

JOURNAL, Unpublished
REFERENCE 3 (bases 1 to 116840)

AUTHORS Simon, M. I.
JOURNAL Unpublished

REFERENCE	AUTHORS	TITLE
4 (bases 1 to 16840)	Cantu, L.A., McBernid, H.E., Simon, M.J. and Roe, B.A.	Direct Submission

Submitted (16-FEB-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma 620 Partlow Hall Room 208 Norman

OK 73019, USA
5 (bases 1 to 116840)

AUTHORS	Cantu, L. A., McDermid, H. E., Simon, M. I., and Roe, B. A.
TITLE	Direct Submission

JOURNAL:	Submitted (14-MAY-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Partington Hall, Room 208, Norman, OK 73019, USA
REFERENCE:	6 (Bases 1 to 16840)
AUTHORS:	Gentile, L.A., Mcdermott, H.E., Simon, M.I. and Kuo, B.A.
TITLE:	Direct Submission
JOURNAL:	Submitted (12-OCT-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Partington Hall, Room 208, Norman, OK 73019, USA
COMMENT:	On May 14, 1999 this sequence version replaced g1:4803972.
FEATURES:	Location/Qualifiers

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Search completed: May 27, 2003, 07:17:59
Job time : 88.1032 secs

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Best Local Similarity 100.0% Pred. No. 33;
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QY 1 TCGTGTGGAGAGAGTGGCAG 20
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Db 1 TCGTGTGGAGAGAGTGGCAG 20

RESULT 2
AR098113 218 bp DNA linear PAT 14 FEB 2001
DEFINITION Sequence 21 from patent US 6074832.
ACCESSION AR098113
VERSION AR098113.1 GI:12807370
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 218)
AUTHORS Ventura, P.J., Brewer, G.J., Yuzbasizyan-Gurkan, V., Schall, W.D. and Duffeck, J.

TITLE DNA encoding canine von Willebrand factor and methods of use
JOURNAL Patent: US 6074832-A 21 13-JUN-2000;
FEATURES location/qualifiers
source 1..218
/organism="unknown"

BASE COUNT 28 a 67 c 74 g 49 t
ORIGIN

Query Match 100.0% Score 20; DB 6; Length 218;
Best Local Similarity 100.0% Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGTGGAGAGAGTGGCAG 20
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Db 2 TCGTGTGGAGAGAGTGGCAG 21

RESULT 3
AF099154 8601 bp mRNA linear MAN 14 JAN 1999
DEFINITION Canis familiaris von Willebrand factor (VWF) mRNA, complete cds.
ACCESSION AF099154
VERSION AF099154.1 GI:4157308
KEYWORDS
SOURCE
ORGANISM Canis familiaris.
Canis familiaris.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 8601)
Schall, W.D.
Ventura, P.J., Li, J., Yuzbasizyan-Gurkan, V., Brewer, G.J. and

REFERENCE 1 (bases 1 to 8601)
AUTHORS Schall, W.D.
TITLE Complete sequence of the structural gene for canine von Willebrand factor and identification of a mutation causing Scottish terrier von Willebrand's disease
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 8601)
AUTHORS Ventura, P.J., Li, J., Yuzbasizyan-Gurkan, V., Brewer, G.J. and Schall, W.D.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1998) Microbiology, Michigan State University,
College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES location/qualifiers
source 1..8601
/organism="Canis familiaris"
/db_xref="taxon:9615"

gene
CDS

1..8601
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Db 659 TCGTGTGGAGAGAGTGGCAG 678
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DOCVWG 8654 bp DNA linear MAN 02-AUG-1996
LOCUS
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Best Local Similarity 100.0% Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT 1825 a 2436 c 2508 g 1832 t
ORIGIN

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 GGQIMTLKRDETIGDCTSHCKYKNHGEVIMKRVKVPPEPFKCTAFGSKIMIP
 CTCDCITCEPECKDITAKLORVKGDCSEEDVIRCEGCKASKAVYSTIHMEDVDD
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BASE COUNT 1825 a 2473 c 2547 g 1849 t

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 8694;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTCTGAGAGTGGCAG 20
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 DB 763 TCTCTGAGAGTGGCAG 782

RESULT 6
 LOCUS AR098096 8802 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 1 from patent US 6074832.
 ACCESSION AR098096
 VERSION AR098096.1 GI:12807353
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 8802)
 AUTHORS Ventap P T, Brewer J J, Yuzhasliyan-Gurkan, V., Schall, W.D. and
 Duitendack, J.
 TITLE DNA encoding canine von Willebrand factor and methods of use
 JOURNAL Patent: US 6074832-A 1-13-JUN-2000;
 FEATURES
 source location/Qualifiers
 1..8802
 /organism="unknown"

BASE COUNT 1886 a 2477 c 2544 g 1895 t

ORIGIN

Query Match 100.0%; Score 20; PP 6; Length 8802;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTCTGAGAGTGGCAG 20
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 DB 861 TCTCTGAGAGTGGCAG 880

RESULT 7
 HMMWFA04 734 bp DNA linear PRI 14-JAN-1995
 LOCUS HMMWFA04 734 bp DNA linear PRI 14-JAN-1995
 DEFINITION Human von Willebrand factor gene, exon 7.
 ACCESSION M25831 M25716
 VERSION M25831.1 GI:34032C
 KEYWORDS
 SPMENT
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Human placenta, leukocyte, fetal liver and cell line EB9 DNA
 clones [lambda- 11,2,7,9,11], h16,7,18], c11,2,3,4,5,9,14,18] and
 pME15,8,123].

REFERENCE 1 (bases 1 to 734)
 AUTHORS Mannes, D. J., Tukey, K. A., Westfield, L. A., Worrall, N. K.,
 Shelton-Indles, B. E., Sorace, J. M., Avery, V. G. and Sadler, J. E.
 TITLE Structure of the gene for human von Willebrand factor
 JOURNAL J. Biol. Chem. 264 (35), 19514-19527 (1989)
 MEDLINE 90062044
 PUBMED 2564182
 COMMENT Draft entry and computer-readable sequence for [1] kindly provided
 by J.E.Sadler, 30-JUN-1989.
 FEATURES
 source location/Qualifiers
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 /db_xref="taxon:9606"
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 109..325
 /gene="VWF"
 /number=7
 326..5734
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BASE COUNT 106 a 247 c 216 g 165 t
 ORIGIN About 13.7 kb after segment 3, chromosome 12pter-p12.

Query Match 95.0%; Score 19; DB 9; Length 734;
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTGTGGAGAGTGGCAG 20
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 DB 111 CCTGTGGAGAGTGGCAG 129

RESULT 8
 LOCUS AY004876 1110 bp mRNA linear MAN 14-JUL-2001
 DEFINITION Sus scrofa von Willebrand Factor precursor (VWF) mRNA, partial cds.
 ACCESSION AY004876
 VERSION AY004876.1 GI:14718399
 KEYWORDS
 SOURCE Sus scrofa.
 ORGANISM Sus scrofa.
 REFERENCE 1 (bases 1 to 1110)
 AUTHORS Fahs, S.A., Nichols, T.C., Seaman, W.T. and Montgomery, R.K.
 TITLE Porcine vWF cDNA - 5' UT and 1st 1032 bp of propeptide
 JOURNAL Unpublished
 2 (bases 1 to 1110)
 REFERENCE Fahs, S.A., Nichols, T.C., Seaman, W.T. and Montgomery, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2000) VWF Biology, Blood Research Institute, P.O.
 Box 2178, Milwaukee, WI 53201 2178, USA
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ORIGIN

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Query Match: 95.0% Score 19; DB 4; length 1110;
Post local similarity 100.0%
Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ACTGTTGACAGTGCAG 20
DB 745 GATGACACAGTGCAG 753

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RESULT 9	SEQUENCE
SWIMMER	4429 bp mRNA linear PRI 21-MAR-1995
LOCUS	Human mRNA fragment (5' terminus) for von Willebrand factor (vWF)
DEFINITION	X04146
ACCESSION	X04146.1 GI:37941
VERSION	1
KEYWORDS	glycoprotein; plasma protein; signal peptide; von Willebrand factor.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Fukuyama; Metazoa; Chordata; Gnathia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini, Hominoidea, Homo.
ATTN	1 (bases 1 to 4429)
TITLE	Willebrand, C.L., Diegaerde, P.J., Hart, M. and Pannekoek, H. Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protein considerably larger than the mature vWF subunit
JOURNAL	EMBO J. 5 (8) 1849-1847 (1986)
MEDLINE	87004550
COMMENT	See also: HSWWF1 (M10221) corresponding to pos. 2458-2842 and HSWWF2 (M10220) corresponding to pos. 4094-4429.
FEATURES	Location/Qualifiers
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[illegible]

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Best Local Similarity 100.0%   From Nucleotide
Matches 19; Mismatched 0; Mismatches
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RESULTS	10
A09265	
LOCUS	720814
DEFINITION	Partial sequence of nucleotide sequence factor derived from human DNA.
ACCESSION	A09265
VERSION	A09265.1 (19940404)
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
ACTIVCS	1 (bases 1 to 7208)
TITLE	Synthetic construct of
JOURNAL	synthetic construct
	artificial sequences.
	1 (bases 1 to 7208)
	Franke, R., H. Vogel, J. L. Franke
	Preparation of the human von Willebrand
	Factor cDNA. <i>Proc Natl Acad Sci USA</i> 91:15061-15064
	1994
	Patent: EP 0629742-A 4 15-06-1994
	Sticht: N. Weinman VAN de, M. H. H. H.
	Leiden/Qualifiers
FEATURES	
SOURCE	

[illegible]

Query Match	95.0%	Score 19	DB 6	Length 7200
Best Local Similarity	100.0%	Prod. No. 48		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 2	CCCTGCTACACATCTCCAC	70		
Db 888	CCCTGTACACATCTCTAC	69		
Result 11				
LOCUS	HSWMFRI	8575 bp	mRNA	linear
DEFINITION	Human mRNA for pre-pro-von Willebrand factor			191 09-JAN-1998
ACCESSION	X03485			
VERSION	X03485.1	GI:17346		
KEYWORDS	glycoprotein; signal peptide; von Willebrand factor.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotic, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
AUTHORS	Bonhuth, D., Orr, E.C., Mitschke, M., Ginsburg, D., Handin, R. I and Orkin, S.H.			
TITLE	Nucleotide sequence of pre-pro-von Willebrand factor cDNA			
JOURNAL	Nucleic Acids Res. 14 (17), 7125-7127 (1986)			
MEDLINE	87016349			
PUBMED	3489923			
REFERENCE	2 (bases 1 to 8575)			
AUTHORS	Eschardt, A.F., Temple, C.S., Deluca, A.W. and Hill, R.L.			
TITLE	The complete cDNA sequence and structural polymorphism of the polypeptide chain of porcine submaxillary mucin			
JOURNAL	J Biol Chem. 272 (52), 33204-33210 (1997)			
MEDLINE	98070526			
PUBMED	9407109			
FEATURES	location/Qualifiers			
source	1. 8575			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			

[illegible]

RESULT 12

LOCUS

108449

Sequence 3 from Patent WO 8606096

DEFINITION

108449.1 G1:588840

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 8588)

Ginsburg, D., Orkin, S. H. and Kaufman, R. J.

WON WILLEBRAND FACTOR

Patent: WO 8606096-A 3 23-OCT-1986

FEATURES

Source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

193

Conservative

0

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

RESULT 14

LOCUS

E01056

CNA gene and the product of human Y

DEFINITION

E01056.1 G1:1196415

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

Homo sapiens (human)

REFERENCE

1 (bases 1 to 8605)

Ginsburg, D., Orkin, S. H. and Kaufman, R. J.

WON WILLEBRAND FACTOR

Patent: WO 8606096-A 3 23-OCT-1986

FEATURES

Source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

193

Conservative

0

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

Score 192

DB 6

Length 8588

Prod. No. 47

Mismatches

0

Indels

0

Gaps

0

REFERENCE
AUTHORS

Mammalia: Primates; Catarrhini; Hominoidea: Homo.
1 (bases 1 to 111904)

REFERENCE
AUTHORS
TITLE

Unpublished

2 (bases 1 to 111904)

Worley, K.C.

Direct Submission

Submitted (22-OCT-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS
TITLE

Unpublished

3 (bases 1 to 111904)

Worley, K.C.

Direct Submission

Submitted (08-JAN-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS
TITLE

Unpublished

4 (bases 1 to 111904)

Worley, K.C.

Direct Submission

Submitted (27-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS
TITLE

Unpublished

5 (bases 1 to 111904)

Worley, K.C.

Direct Submission

Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect = 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards. Estimated error rate is less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu/robr/quality/info/genbank.annotation.html>.

QUALSTAT-REPORT

Summary Statistics

Contig length: 94462

Phrap values in estimate: 93326

Average error rate (BCM-Phrap estimate): 0.000923054

Fraction of Phrap values less than 40: 0.045195

Number of consensus changing edits: 3

Number of N's in consensus: 0

Consensus changing edits

Position	Original/Context	Edited/Context
19379	agagcttaaa(g)acacaggttc	agagcttaaa(g)acacaggttc
29991	tttaagtaga(a)atagaggttc	tttaagtaga(a)atagaggttc
89256	gcacggagctt(t)ctctggccca	gcacggagctt(t)ctctggccca

Distribution of Quality < 40 Bases

# bases	5	10	15	20	25	30	35	40
10001								*
9001								*
8001								*
7001								*
6001								*
5001								*
4001								*
3001			*	*	*	*	*	*
2001		*	*	*	*	*	*	*
1001	*	*	*	*	*	*	*	*
01								

Phrap Value Range

FEATURES

source

Version: 1.01 qxto.

location/Qualifiers

1..111904

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/db_xref="taxon:9606"

/chromosome="12"

/clone="RPC13-467F14"

43..319

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complement(783..1081)

/rpl_family="A1u5x"

complement(1109..1249)

/rpl_family="12"

complement(1250..1412)

/rpl_family="MER5A"

1962..2258

/rpl_family="A1u5x"

complement(2816..3008)

/rpl_family="A1u5p"

4761..4911

/rpl_family="MER20"

5307..5504

/rpl_family="A1u50"

5990..6043

/rpl_family="MER"

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repeat_region 7053, .7347
                /rpl_family="AluY"
repeat_region complement(7736, .7841)
                /rpl_family="(A)n"
repeat_region complement(8668, .8976)
                /rpl_family="AluY"
repeat_region 9030, .9259
                /rpl_family="AluB"
repeat_region complement(9835, .9910)
                /rpl_family="MIR"
repeat_region 10696, .10991
                /rpl_family="AluY"
repeat_region complement(11228, .11294)
                /rpl_family="LIM4"
repeat_region complement(11428, .11542)
                /rpl_family="FLAM_A"
repeat_region complement(11646, .11945)
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repeat_region complement(12278, .12316)
                /rpl_family="(CA)n"
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misc_feature 12677, .12817
                /function="low coverage"
repeat_region 12688, .12974
                /rpl_family="AluY"
repeat_region complement(13020, .13203)
                /rpl_family="LIM4"
repeat_region complement(13222, .13689)
                /rpl_family="LIME1"
repeat_region complement(13750, .14053)
                /rpl_family="AluS4"
repeat_region complement(14054, .14412)
                /rpl_family="LIM3"
repeat_region complement(14440, .14585)
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repeat_region complement(14586, .14889)
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repeat_region 15110, .15408
                /rpl_family="AluX"

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Query Match          95.0% Score 19; DB 9; length 11904;
Best local Similarity 100.0%; Pred.No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 CTTGTGGAGACAGTGCAC 20
        |||
Db 45096 CTTGTGGAGACAGTGCAC 45114

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Search completed: May 27, 2003, 07:17:17
 Job time : 75.0777 secs

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